

C1

V1

	101						150
EG327	GVLTAGTITL	KAGDNLKIQ	NTNENTNASSFTYSLK	KDLTDLTSVG		
BZ198	RVLKAGAITL	KAGDNLKIQ	NTNENTNDSSFTYSLK	KDLTDLTSVE		
BZ10	RVLKAGAITL	KAGDNLKIQ	NTNENTNENT	NDSSFTYSLK	KDLTDLTSVE		
H15	RVLKAGAITL	KAGDNLKIQ	NTNENTNENT	NDSSFTYSLK	KDLTDLTSVE		
EG329	GVLTAAREITL	KAGDNLKIQ	NG...TN...FTYSLK	KDLTDLTSVG		
PMC21	GVLTAAREITL	KAGDNLKIQ	NG...TN...FTYSLK	KDLTDLTSVG		
H38	NTLHGATVTL	KAGDNLKIQ	NTNKNTNENT	NDSSFTYSLK	KDLTDLTSVE		
P20	TLHG.ATVTL	KAGDNLKIQ	SGKD.....FTYSLK	KELKDLTSVE		
Z2491	FVDPYIVVTL	KAGDNLKIQ	NTNENTNASSFTYSLK	KDLTGLINVE		
H41	FVDPYIVVTL	KAGDNLKIQ	NTNENTNASSFTYSLK	KDLTGLINVE		
Consensus	-----TL	<u>KAGDNLKIQ</u>	-----	----FTYSLK	K-L--L--V-		
	V1	C2	V2		C3		

	151		200
EG327	TEKLSFSANS	NKVNITSDTK	GLNFAKKTAE TNGDPTVHLN GIGSTLTDTL
BZ198	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
BZ10	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
H15	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
EG329	TEKLSFSANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
PMC21	TEKLSFSANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
H38	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
P20	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
Z2491	TEKLSFGANG	KKVNIISDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
H41	TEKLSFGANG	KKVNIISDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
Consensus	TEKLSF-AN-	-KVNI-SDTK	GLNFAK-TA- TNGD-TVHLN GIGSTLTD-L

C3

	201		250
EG327	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN AGWNIKGVP GTTAS..DNV
BZ198	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN AGWNIKGVP GTTAS..DNV
BZ10	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN AGWNIKGVP GTTAS..DNV
H15	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN AGWNIKGVP GTTAS..DNV
EG329	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN AGWNIKGVP GTTAS..DNV
PMC21	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN AGWNIKGVP GTTAS..DNV
H38	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN AGWNIKGVP GTTAS..DNV
P20	AGSSASHVDA	GNQST..HYT	RAASIKDVLN AGWNIKGVP GTTAS..DNV
Z2491	AGSSASHVDA	GNQST..HYT	RAASIKDVLN AGWNIKGVP GTTAS..DNV
H41	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN AGWNIKGVP GTTAS..DNV
Consensus	----A-----	----T-----	RAAS-KDVLN AGWNIKGVP G-T-----NV

V3

C4

V4

	251		300
EG327	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK RTEVKIGAKT SVIKEKDGL
BZ198	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK RTEVKIGAKT SVIKEKDGL
BZ10	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK RTEVKIGAKT SVIKEKDGL
H15	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK RTEVKIGAKT SVIKEKDGL
EG329	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK RTEVKIGAKT SVIKEKDGL
PMC21	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK RTEVKIGAKT SVIKEKDGL
H38	DFVHTYDTVE	FLSADTKTTT	VNVESKDNGK RTEVKIGAKT SVIKEKDGL
P20	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK RTEVKIGAKT SVIKEKDGL
Z2491	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK RTEVKIGAKT SVIKEKDGL
H41	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK RTEVKIGAKT SVIKEKDGL
Consensus	DFV-TYDTVE	FLSADTKTTT	VNVESKDNGK -TEVKIGAKT SVIKEKDGL

C5

FIG. 1

	301		350
EG327	VTGKDKGEND	SSTDKEGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGQADK
BZ198	VTGKDKDENG	SSTDKEGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGQADK
BZ10	VTGKDKGEND	SSTDKEGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGQADK
H15	VTGKDKDENG	SSTDKEGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGQADK
EG329	VTGKDKGEND	SSTDKEGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGQADK
PMC21	VTGKDKGEND	SSTDKEGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGQADK
H38	VTGKDKGEND	SSTDKEGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGQADK
P20	VTGKDKGEND	SSTDKEGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGQADK
Z2491	VTGKDKGEND	SSTDKEGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGQADK
H41	VTGKDKGEND	SSTDKEGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGQADK
Consensus	<u>VTGK-K-EN-</u>	<u>SSTD-GEGLV</u>	<u>TAKEVIDAVN KAGWRMKT TT ANGQTGQADK</u>

C5

	351		400
EG327	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI TVMYDVNVGD ALNVNQLQNS
BZ198	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
BZ10	FETVTSGTKV	TFASGNGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
H15	FETVTSGTKV	TFASGNGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
EG329	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI TVMYDVNVGD ALNVNQLQNS
PMC21	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI TVMYDVNVGD ALNVNQLQNS
H38	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
P20	FETVTSGTKV	TFASGNGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
Z2491	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI TVMYDVNVGD ALNVNQLQNS
H41	FETVTSGTKV	TFASGNGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
Consensus	<u>FETVTSGT-V</u>	<u>TFASG-GTTA</u>	<u>TVSKDDQGNI TV-YDVNVGD ALNVNQLQNS</u>

C5

	401		450
EG327	GWNLDKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
BZ198	GWNLDKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
BZ10	GWNLDKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
H15	GWNLDKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
EG329	GWNLDKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
PMC21	GWNLDKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
H38	GWNLDKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
P20	GWNLDKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
Z2491	GWNLDKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EISRNGKNID
H41	GWNLDKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
Consensus	<u>GWNLDKAVA</u>	<u>GSSGKVISGN</u>	<u>VSPSKGKMDE TVNINAGNNI EI-RNGKNID</u>

C5

FIG. 1

451 500

EG327	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
BZ198	IATSMAPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDTNK	PVRITNVAPG
BZ10	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
H15	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
EG329	IATSMTPQFS	SVSLGAGADA	PTLSVDG.DA	LNVGSKKDNK	PVRITNVAPG
PMC21	IATSMTPQFS	SVSLGAGADA	PTLSVDG.DA	LNVGSKKDNK	PVRITNVAPG
H38	IATSMTPQFS	SVSLGAGADA	PTLSVDDKGA	LNVGSKDANK	PVRITNVAPG
P20	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
Z2491	IATSMAPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
H41	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
Consensus	<u>IATSM-PQFS</u>	<u>SVSLGAGADA</u>	<u>PTLSVD---A</u>	<u>LNVGSK--NK</u>	<u>PVRITNVAPG</u>

C5

501 550

EG327	VKEGDVTNVA	QLKGVAQNLN	NHIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
BZ198	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
BZ10	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLAQAYLPG
H15	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLAQAYLPG
EG329	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
PMC21	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
H38	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
P20	VKEGDVTNVA	QLKGVAQNLN	NRIDNVNGNA	RAGIAQAIAT	AGLAQAYLPG
Z2491	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
H41	VKEGDVTNVA	QLKGVAQNLN	NRIDNVNGNA	RAGIAQAIAT	AGLVQAYLPG
Consensus	<u>VKEGDVTNVA</u>	<u>QLKGVAQNLN</u>	<u>N-IDNV-GNA</u>	<u>RAGIAQAIAT</u>	<u>AGL-QAYLPG</u>

C5

551 600

EG327	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
BZ198	KSMMAIGGDT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
BZ10	KSMMAIGGGT	YRGEAGYAIG	YSSISDTGNW	VIKGTASGNS	RGHFGTSASV
H15	KSMMAIGGGT	YRGEAGYAIG	YSSISDTGNW	VIKGTASGNS	RGHFGASASV
EG329	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
PMC21	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
H38	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
P20	KSMMAIGGGT	YLGEAGYAIG	YSSISDTGNW	VIKGTASGNS	RGHFGTSASV
Z2491	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
H41	KSMMAIGGGT	YLGEAGYAIG	YSSISAGGNW	IIKGTASGNS	RGHFGASASV
Consensus	<u>KSMMAIGG-T</u>	<u>Y-GEAGYAIG</u>	<u>YSSIS--GNW</u>	<u>-IKGTASGNS</u>	<u>RGHFG-SASV</u>

C5

FIG. 1

	601
EG327	GYQW.
BZ198	GYQW.
BZ10	GYQW.
H15	GYQW.
EG329	GYQW.
PMC21	GYQW.
H38	GYQW.
P20	GYQW.
Z2491	GYQW.
H41	GYQW.
Consensus	<u>GYQW.</u>
	C5

FIG. 1

	1						70
H15	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC
BZ10	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC
BZ198	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC
P20	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	AGTCGTATCC	GAGCTCACAC
H38	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGCCGTATCC	GAGCTCACAC
Z2491	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGCCGTATCC	GAGCTCACAC
H41	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGCCGTATCC	GAGCTCACAC
EG329	ATGAACGAAA	TATTGCGCAT	CATTGGAAT	AGCGCCCTCA	ATGCCTGGGT	CGTTGTATCC	GAGCTCACAC
PMC21	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCATGGGT	CGTCGTATCC	GAGCTCACAC
EG327	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGCCGTATCC	GAGCTCACAC
Consensus	<u>ATGAAC-AAA</u>	<u>TAT--CGCAT</u>	<u>CATTGGAAT</u>	<u>AG-GCCCTCA</u>	<u>ATGC-TGGGT</u>	<u>-G--GTATCC</u>	<u>GAGCTCACAC</u>

C1

	71						140
H15	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT
BZ10	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT
BZ198	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT
P20	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGCTGT	CCGCAACGGT
H38	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGAAGACCGC	CGTATTGGCG	ACGCTGTTGT	TTGCAACGGT
Z2491	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGAAGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT
H41	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGAAGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT
EG329	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGAAGACCGC	CGTATTGGCG	ACTCTGTTGT	TTGCAACGGT
PMC21	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGAAGACCGC	CGTATTGGCG	ACTCTGTTGT	TTGCAACGGT
EG327	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT
Consensus	<u>GCAACCACAC</u>	<u>CAAACGCGCC</u>	<u>TCCGCAACCG</u>	<u>TG--GACCGC</u>	<u>CGTATTGGCG</u>	<u>AC-CTG-TGT</u>	<u>--GCAACGGT</u>

C1

	141						210
H15	TCAGGCGAAT	GCTACCGATG	ACGAC.....GATTTA	TATTTAGAAC	CCGTACAACG	CACTGCTGTC
BZ10	TCAGGCGAAT	GCTACCGATG	ACGAC.....GATTTA	TATTTAGAAC	CCGTACAACG	CACTGCTGTC
BZ198	TCAGGCGAAT	GCTACCGATG	ACGAC.....GATTTA	TATTTAGAAC	CCGTACAACG	CACTGCTGTC
P20	TCAGGCGAAT	GCTACCGATA	CCGAT.....	.GAAGATGAA	GAGTTAGAA	CCGTAGCACG	CTCTGCTCTG
H38	TCAGGCGAAT	GCTACCGATG	AAGAT.....	.GAAGAAGAA	GAGTTAGAAC	CCGTAGTACG	CTCTGCTCTG
Z2491	TCAGGCGAAT	GCTACCGATG	AAGAT.....	.GAAGAAGAA	GAGTTAGAA	CCGTACAACG	CTCTGTCTGTA
H41	TCAGGCGAAT	GCTACCGATG	AAGAT.....	.GAAGAAGAA	GAGTTAGAA	CCGTACAACG	CTCTG...TC
EG329	TCAGGCAAGT	GCTAACAATG	AAGAGCAAGA	AGAAGATTTA	TATTTAGACC	CCGTGCTACG	CACTGTTGCC
PMC21	TCAGGCAAGT	GCTAACAATG	AAGAGCAAGA	AGAAGATTTA	TATTTAGACC	CCGTACAACG	CACTGTTGCC
EG327	TCAGGCGAGT	ACTACCGATG	ACGAC.....GATTTA	TATTTAGAAC	CCGTACAACG	CACTGCTGTC
Consensus	<u>TCAGGC-A-T</u>	<u>-CTA-C-AT-</u>	<u>--GA-----</u>	<u>----GA---A</u>	<u>-A-TTAGA--</u>	<u>CCGT---ACG</u>	<u>C-CTG----</u>

C1

V1

FIG. 2

211 280

H15	GTGTTGAGCT	TCCGTTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGGTAC	AGAAGA...T	TCAAATTGGG
BZ10	GTGTTGAGCT	TCCGTTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGGTAC	AGAAGA...T	TCAAATTGGG
BZ198	GTGTTGAGCT	TCCGTTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGGTAC	AGAAGA...T	TCAAATTGGG
P20	GTGTTGCAAT	TCATGATCGA	TAAAGAAGGC	AATGGAGAAA	TCGAATCTAC	AGGAGA...T	ATAGGTTGGA
H38	GTGTTGCAAT	TCATGATCGA	TAAAGAAGGC	AATGGAGAAA	ACGAATCTAC	AGGAAA...T	ATAGGTTGGA
Z2491	GGG..AGCAT	TCAAG.CCAG	TATGGAAGGC	AGCGGC GAAT	TGGAAACGAT	ATCAT...T	ATCAATGACT
H41	GTAGGGAGCA	TTCAAGCCAG	TATGGAAGGC	AGCGTCGAAT	TGGAAACGAT	A.....	TCATTATCAA
EG329	GTGTTGATAG	TCAATTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAAAAGT	AGAAGAAAAT	TCAGATTGGG
PMC21	GTGTTGATAG	TCAATTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAAAAGT	AGAAGAAAAT	TCAGATTGGG
EG327	GTGTTGAGCT	TCCGTTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGTTAC	AGAAGA...T	TCAAATTGGG
Consensus	G-----	T-----C--	TA--GAAGGC	A--G--GAA-	--GAA-----	A-----	-----

V1

281 350

H15	CAGTATATTT	CGACGAGAAA	AGAGTACTAA	AAGCCGGAGC	AATCACCCCTC	AAAGCCGGCG	ACAACCTGAA
BZ10	CAGTATATTT	CGACGAGAAA	AGAGTACTAA	AAGCCGGAGC	AATCACCCCTC	AAAGCCGGCG	ACAACCTGAA
BZ198	CAGTATATTT	CGACGAGAAA	AGAGTACTAA	AAGCCGGAGC	AATCACCCCTC	AAAGCCGGCG	ACAACCTGAA
P20	GTATATATTA	CGACGATCAC	AACACTCTAC	ACGGCGCAAC	CGTTACCCTC	AAAGCCGGCG	ACAACCTGAA
H38	GTATATATTA	CGACAATCAC	AACACTCTAC	ACGGCGCAAC	CGTTACCCTC	AAAGCCGGCG	ACAACCTGAA
Z2491	AACGACAGCA	AGGAATTTGT	AGACCCATAC	ATAGTA...	.GTTACCCTC	AAAGCCGGCG	ACAACCTGAA
H41	TGACTAACGA	CAGCAAGGAA	TTTGTAGACC	CATACATAGT	AGTTACCCTC	AAAGCCGGCG	ACAACCTGAA
EG329	CAGTATATTT	CAACGAGAAA	GGAGTACTAA	CAGCCAGAGA	AATCACCCCTC	AAAGCCGGCG	ACAACCTGAA
PMC21	CAGTATATTT	CAACGAGAAA	GGAGTACTAA	CAGCCAGAGA	AATCACCCCTC	AAAGCCGGCG	ACAACCTGAA
EG327	GAGTATATTT	CGACAAGAAA	GGAGTACTAA	CAGCCGGAAC	AATCACCCCTC	AAAGCCGGCG	ACAACCTGAA
Consensus	-----A---	-----	-----	-----	--T-ACCCTC	AAAGCCGGCG	ACAACCTGAA

V1

C2

351 420

H15	AATCAAACAA	AACACCAATG	AAAACACCAA	TGAAAACACC	AATGACAGTA	GCTTCACCTA	CTCCCTGAAA
BZ10	AATCAAACAA	AACACCAATG	AAAACACCAA	TGAAAACACC	AATGACAGTA	GCTTCACCTA	CTCCCTGAAA
BZ198	AATCAAACAA	AACACCAATG	AAAACACC..	AATGACAGTA	GCTTCACCTA	CTCCCTGAAA
P20	AATCAAACAA	AGCGGCAAG	A.....CTTCACCTA	CTCGCTGAAA
H38	AATCAAACAA	AACACCAATA	AAAACACCAA	TGAAAACACC	AATGACAGTA	GCTTCACCTA	CTCGCTGAAA
Z2491	AATCAAACAA	AACACCAATG	AAAACACC..	AATGCCAGTA	GCTTCACCTA	CTCGCTGAAA
H41	AATCAAACAA	AACACCAATG	AAAACACC..	AATGCCAGTA	GCTTCACCTA	CTCGCTGAAA
EG329	AATCAAACAA	AAC.....G..GCACAA	ACTTCACCTA	CTCGCTGAAA
PMC21	AATCAAACAA	AAC.....G..GCACAA	ACTTCACCTA	CTCGCTGAAA
EG327	AATCAAACAA	AACACCAATG	AAAACACC..	AATGCCAGTA	GCTTCACCTA	CTCGCTGAAA
Consensus	AATCAAACAA	A-C-----	-----	-----	-----	-CTTCACCTA	CTC-CTGAAA

C2

V2

C3

FIG. 2

421 490

H15	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGT	AATAAAGTCA
BZ10	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGT	AATAAAGTCA
BZ198	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGT	AATAAAGTCA
P20	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGT	AATAAAGTCA
H38	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGT	AATAAAGTCA
Z2491	AAAGACCTCA	CAGGCCTGAT	CAATGTTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGC	AAGAAAGTCA
H41	AAAGACCTCA	CAGGCCTGAT	CAATGTTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGC	AAGAAAGTCA
EG329	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGC	AAGAAAGTCA
PMC21	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGC	AATAAAGTCA
EG327	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGC	AATAAAGTCA
Consensus	<u>AAAGA-CT-A</u>	<u>-AG--CTGA-</u>	<u>CA-TGTTG-A</u>	<u>ACTGAAAAAT</u>	<u>TATCGTTT-G</u>	<u>CGCAAAC-G-</u>	<u>AA-AAAGTCA</u>

C3

491 560

H15	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT
BZ10	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT
BZ198	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT
P20	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT
H38	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT
Z2491	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT
H41	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT
EG329	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT
PMC21	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT
EG327	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT
Consensus	<u>ACATCA-AAG</u>	<u>CGACACCAAA</u>	<u>GGCTTGAATT</u>	<u>T-GCGAAA-A</u>	<u>AACGGCTG-G</u>	<u>AC-AACGGCG</u>	<u>A-C-CCACGGT</u>

C3

561 630

H15	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC
BZ10	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC
BZ198	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC
P20	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC
H38	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC
Z2491	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC
H41	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC
EG329	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC
PMC21	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC
EG327	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC
Consensus	<u>TCATCTGAAC</u>	<u>GGTAT-GGTT</u>	<u>CGACTTTGAC</u>	<u>CGATA-GCT-</u>	<u>--G--T-C--</u>	<u>--GC--C---</u>	<u>----G---C-</u>

C3

V3

FIG.2

	631						700
H15	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGC GGCAA	GCGTTAAAGA	CGTATTAAAC	GCAGGCTGGA
BZ10	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGC GGCAA	GCGTTAAAGA	CGTATTAAAC	GCAGGCTGGA
BZ198	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGC GGCAA	GCGTTAAAGA	CGTATTAAAC	GCAGGCTGGA
P20	GGTAACCAAA	GTACACATTA	C.....ACT	CGTGCAGCAA	GTATTAAGGA	TGTGTTGAAT	GCGGGTTGGA
H38	AACGACAACG	TTACCGATGA	CAAGAAAAAA	CGTGC GGCAA	GCGTTAAAGA	CGTATTAAAC	GCAGGCTGGA
Z2491	GGTAACCAAA	GTACACATTA	C.....ACT	CGTGCAGCAA	GTATTAAGGA	TGTGTTGAAT	GCGGGTTGGA
H41	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGC GGCAA	GCGTTAAAGA	CGTATTAAAC	GCAGGCTGGA
EG329	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGC GGCAA	GCGTTAAAGA	CGTATTAAAC	GCTGGCTGGA
PMC21	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGC GGCAA	GCGTTAAAGA	CGTATTAAAC	GCTGGCTGGA
EG327	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGC GGCAA	GCGTTAAAGA	CGTATTAAAC	GCAGGCTGGA
Consensus	---AC-A--	-TAC--AT-A	C-----A--	CGTGC-GCAA	G--TTAA-GA	-GT-TT-AA-	GC-GG-TGGA
		V3			C4		
	701						770
H15	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACTTACGA
BZ10	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTC	GATTTCGTCC	GCACTTACGA
BZ198	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACTTACGA
P20	ATATTAAGGG	TGTTAAAACT	GGCTCAACAA	CTGGTCAATC	AGAAAATGTC	GATTTCGTCC	GCACTTACGA
H38	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	ACACTTACGA
Z2491	ATATTAAGGG	TGTTAAAACT	GGCTCAACAA	CTGGTCAATC	AGAAAATGTC	GATTTCGTCC	GCACTTACGA
H41	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACTTACGA
EG329	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACTTACGA
PMC21	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACTTACGA
EG327	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACTTACGA
Consensus	A-ATTAA-GG	-GTTAAA-C-	GG--CAACA-	CT-----TC	-GA-AA-GT-	GATTTCGTCC	-CACTTACGA
	C4		V4			C5	
	771						840
H15	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
BZ10	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
BZ198	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
P20	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
H38	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
Z2491	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
H41	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
EG329	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
PMC21	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
EG327	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
Consensus	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
				C5			
	841						910
H15	AAAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
BZ10	AGAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
BZ198	AAAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
P20	AGAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
H38	AGAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
Z2491	AGAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
H41	AAAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
EG329	AAAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
PMC21	AAAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
EG327	AGAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATCA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
Consensus	A-AACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTAT-A	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
				C5			

FIG. 2

911 980

H15	AAGGCAAAGA	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
BZ10	AAGGCAAAGG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
BZ198	AAGGCAAAGA	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
P20	AAGGCAAAGG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
H38	AAGGCAAAGG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
Z2491	AAGGCAAAGG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
H41	AAGGCAAAGG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
EG329	AAGACAAAGG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
PMC21	AAGACAAAGG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
EG327	AAGACAAAGG	CGAGAATGAT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
Consensus	AAG-CAAAG-	CGAGAATG-T	TCTTCTACAG	AC-AAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA

C5

981 1050

H15	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
BZ10	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
BZ198	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
P20	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
H38	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
Z2491	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
H41	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
EG329	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
PMC21	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
EG327	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
Consensus	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG

C5

1051 1120

H15	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTGCG	ACTGTAAGTA
BZ10	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTGCG	ACTGTAAGTA
BZ198	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTGCG	ACTGTAAGTA
P20	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTGCG	ACTGTAAGTA
H38	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTGCG	ACTGTAAGTA
Z2491	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTGCG	ACTGTAAGTA
H41	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTGCG	ACTGTAAGTA
EG329	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTGCG	ACTGTAAGTA
PMC21	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTGCG	ACTGTAAGTA
EG327	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTGCG	ACTGTAAGTA
Consensus	TTTGAAACCG	TTACATCAGG	CACAAA-GTA	ACCTTTGCTA	GTGGTAA-GG	TACAACCTGCG	ACTGTAAGTA

C5

1121 1190

H15	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
BZ10	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
BZ198	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
P20	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
H38	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
Z2491	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
H41	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
EG329	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
PMC21	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
EG327	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
Consensus	AAGATGATCA	AGGCAACATC	ACTGTTA-GT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT

C5

FIG. 2

1191 1260

H15	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
BZ10	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
BZ198	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
P20	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
H38	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
Z2491	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
H41	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
EG329	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
PMC21	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
EG327	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
Consensus	<u>GCAAAACAGC</u>	<u>GGTTGGAATT</u>	<u>TGGATTCCAA</u>	<u>AGCGGTTGCA</u>	<u>GGTCTTCGG</u>	<u>GCAAAGTCAT</u>	<u>CAGCGGCAAT</u>

C5

1261 1330

H15	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
BZ10	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
BZ198	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
P20	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
H38	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
Z2491	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
H41	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
EG329	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
PMC21	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
EG327	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
Consensus	<u>GTTTCGCCGA</u>	<u>GCAAGGGAAA</u>	<u>GATGGATGAA</u>	<u>ACCGTCAACA</u>	<u>TTAATGCCGG</u>	<u>CAACAACATC</u>	<u>GAGATTACCC</u>

C5

1331 1400

H15	GCAACGGCAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGGCGCGGG
BZ10	GCAACGGCAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGGCGCGGG
BZ198	GCAACGGTAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGGCGCGGG
P20	GCAACGGCAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGGCGCGGG
H38	GCAACGGTAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGGCGCGGG
Z2491	GCAACGGTAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGGCGCGGG
H41	GCAACGGCAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGGCGCGGG
EG329	GCAACGGTAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGGCGCGGG
PMC21	GCAACGGTAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGGCGCGGG
EG327	GCAACGGCAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGGCGCGGG
Consensus	<u>GCAACGG-AA</u>	<u>AAATATCGAC</u>	<u>ATCGCCACTT</u>	<u>CGATG-C-CC</u>	<u>GCA-TTTTCC</u>	<u>AGCGTTTCGC</u>	<u>TCGG-CGCGG</u>

C5

1401 1470

H15	GGCGGATGCG	CCCACTTTAA	GCGTGGATGA	CGAGGGCGCG	TTGAATGTCG	GCAGCAAGGA	TGCCAACAAA
BZ10	GGCGGATGCG	CCCACTTTAA	GCGTGGATGA	CGAGGGCGCG	TTGAATGTCG	GCAGCAAGGA	TGCCAACAAA
BZ198	GGCGGATGCG	CCCACTTTGA	GCGTGGATGA	CGAGGGCGCG	TTGAATGTCG	GCAGCAAGGA	TGCCAACAAA
P20	GGCGGATGCG	CCCACTTTAA	GCGTGGATGA	CGAGGGCGCG	TTGAATGTCG	GCAGCAAGGA	TGCCAACAAA
H38	GGCGGATGCG	CCCACTTTGA	GCGTGGATGA	CGAGGGCGCG	TTGAATGTCG	GCAGCAAGGA	TGCCAACAAA
Z2491	GGCAGATGCG	CCCACTTTAA	GCGTGGATGA	CGAGGGCGCG	TTGAATGTCG	GCAGCAAGGA	TGCCAACAAA
H41	GGCGGATGCG	CCCACTTTAA	GCGTGGATGA	CGAGGGCGCG	TTGAATGTCG	GCAGCAAGGA	TGCCAACAAA
EG329	GGCGGATGCG	CCCACTTTGA	GCGTGGAT..	GGGGACGCA	TTGAATGTCG	GCAGCAAGAA	GGACAACAAA
PMC21	GGCGGATGCG	CCCACTTTGA	GCGTGGAT..	GGGGACGCA	TTGAATGTCG	GCAGCAAGAA	GGACAACAAA
EG327	GGCGGATGCG	CCCACTTTAA	GCGTGGATGA	CGAGGGCGCG	TTGAATGTCG	GCAGCAAGGA	TGCCAACAAA
Consensus	<u>GGC-GATGCG</u>	<u>CCCACTTT-A</u>	<u>GCGTGGAT--</u>	<u>---GG-CGC-</u>	<u>TTGAATGTCG</u>	<u>GCAGCAAG-A</u>	<u>---CAACAAA</u>

C5

FIG. 2

12/31

	1471							1540
H15	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG	
BZ10	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG	
BZ198	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG	
P20	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG	
H38	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG	
Z2491	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG	
H41	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCG	CAACTTAAAG	
EG329	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG	
PMC21	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG	
EG327	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG	
Consensus	<u>CCCGTCCGCA</u>	<u>TTACCAATGT</u>	<u>CGCCCCGGGC</u>	<u>GTTAAAGAGG</u>	<u>GGGATGTTAC</u>	<u>AAACGTCGC-</u>	<u>CAACTTAAAG</u>	

C5

	1541							1610
H15	GTGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGCGCGGGTA	TCGCCCAAGC	
BZ10	GTGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGCGCGGGTA	TCGCCCAAGC	
BZ198	GCGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGTGC GGGA	TCGCCCAAGC	
P20	GTGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGCGCGGGTA	TCGCCCAAGC	
H38	GCGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGTGC GGGA	TCGCCCAAGC	
Z2491	GCGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGTGC GGGA	TCGCCCAAGC	
H41	GTGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGTGC GGGA	TCGCCCAAGC	
EG329	GCGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGTGC GGGA	TCGCCCAAGC	
PMC21	GCGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGTGC GGGA	TCGCCCAAGC	
EG327	GCGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGTGC GGGA	TCGCCCAAGC	
Consensus	<u>G-GTGGCGCA</u>	<u>AAACTTGAAC</u>	<u>AACC-CATCG</u>	<u>ACAATGTG-A</u>	<u>CGGCAACGCG</u>	<u>CG-GCGGG-A</u>	<u>TCGCCCAAGC</u>	

C5

	1611							1680
H15	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGTACT	
BZ10	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGTACT	
BZ198	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGACT	
P20	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGTACT	
H38	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGACT	
Z2491	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGACT	
H41	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGACT	
EG329	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGACT	
PMC21	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGACT	
EG327	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGACT	
Consensus	<u>GATTGCAACC</u>	<u>GCAGGT-T-G</u>	<u>-TCAGGC-TA</u>	<u>T-TGCCCGGC</u>	<u>AAGAGTATGA</u>	<u>TGGCGATCGG</u>	<u>CGGCG--ACT</u>	

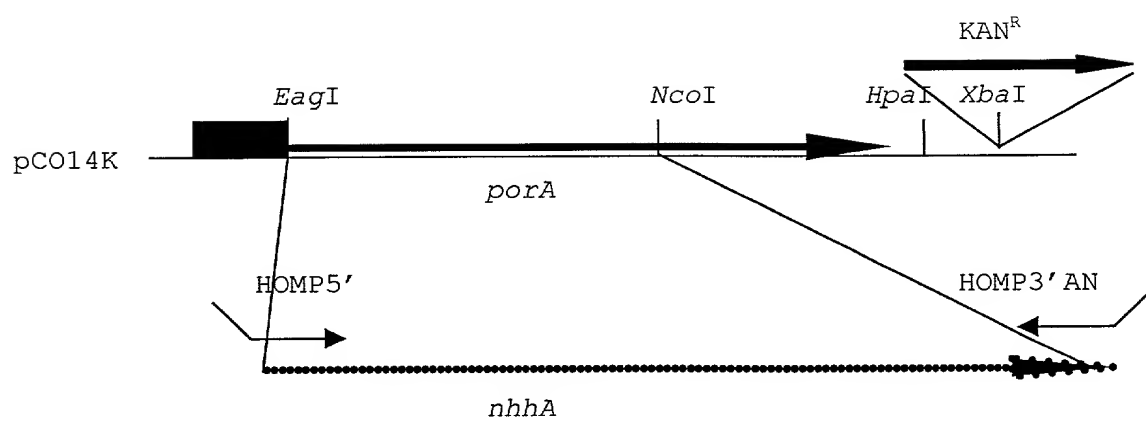
C5

FIG. 2

FIG. 2

	1751		1815				
H15	GCAcGGCTTC	CGGCAATTcG	CGGGCCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAGT	1815
BZ10	GCACGGCTTC	CGGCAATTcG	CGCGGTcATT	TCGGTACTTC	CGCATCTGTC	GGTTATCAGT	GGTAA
BZ198	GCACGGCTTC	CGGCAATTcG	CGGGCCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAAT	GGTAA
P20	GCACGGCTTC	CGGCAATTcG	CGGGTcATT	TCGGTACTTC	CGCATCTGTC	GGTTATCAGT	GGTAA
H38	GCACGGCTTC	CGGCAATTcG	CGGGTcATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAGT	GGTAA
Z2491	GCACGGCTTC	CGGCAATTcG	CGGGCCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAGT	GGTAA
H41	GCACGGCTTC	CGGCAATTcG	CGGGCCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAGT	GGTAA
EG329	GCACGGCTTC	CGGCAATTcG	CGGGCCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAGT	GGTAA
PMC21	GCACGGCTTC	CGGCAATTcG	CGGGCCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAGT	GGTAA
EG327	GCACGGCTTC	CGGCAATTcG	CGGGCCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAGT	GGTAA
Consensus	GCACGGCTTC	CGGCAATTcG	CGGG-CATT	TCGGT-CTTC	CGCATCTGTC	GGTTATCA-T	GGTAA

C5

**FIG. 3A**

PIP52 (PMC21)

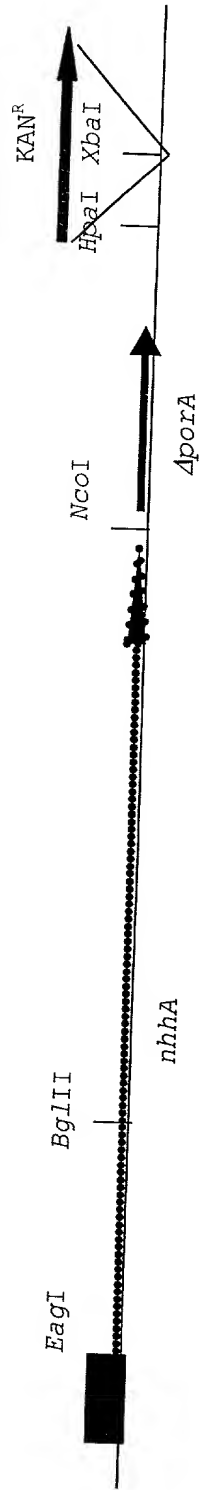


FIG. 3B



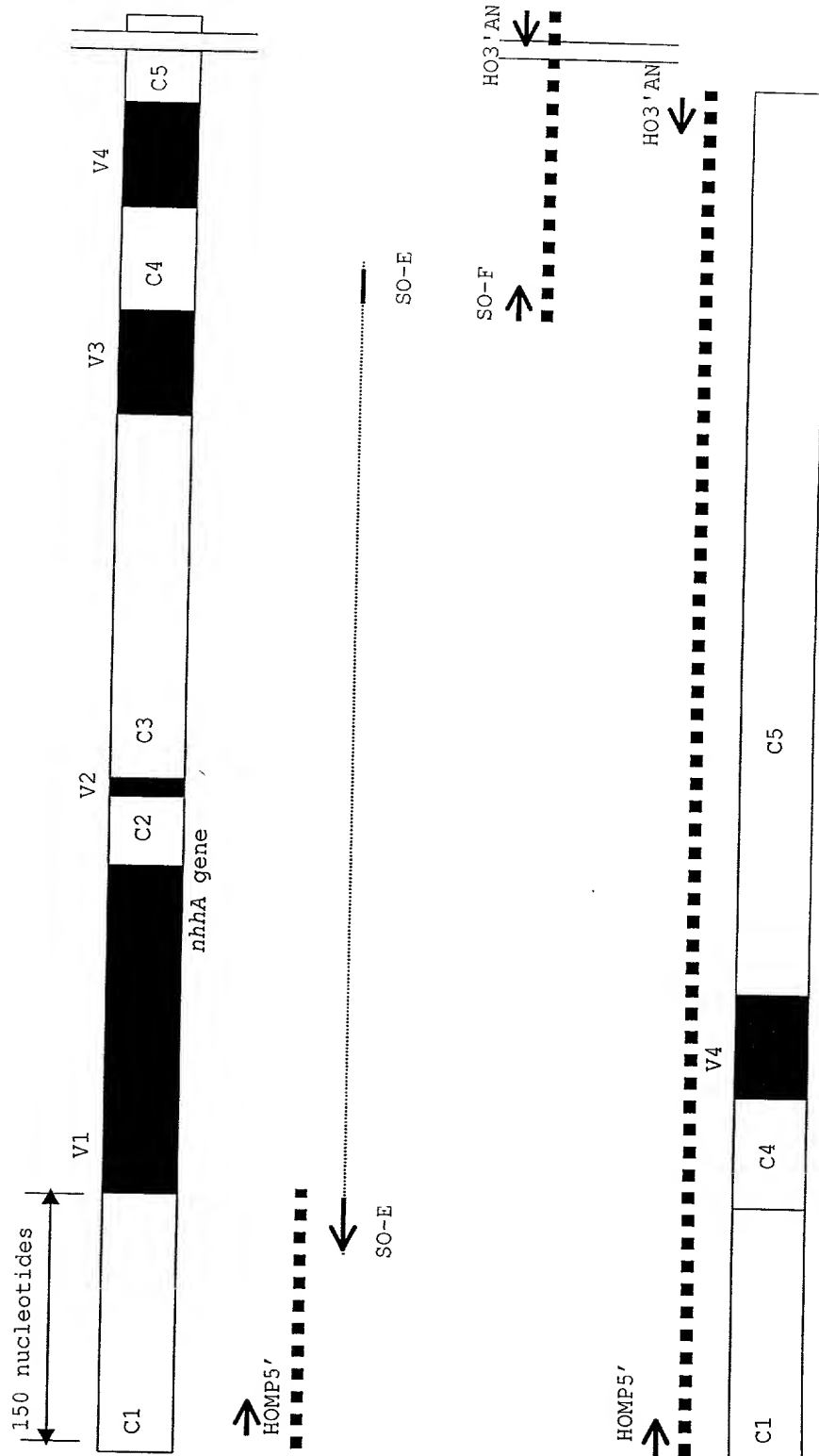


FIG. 4B

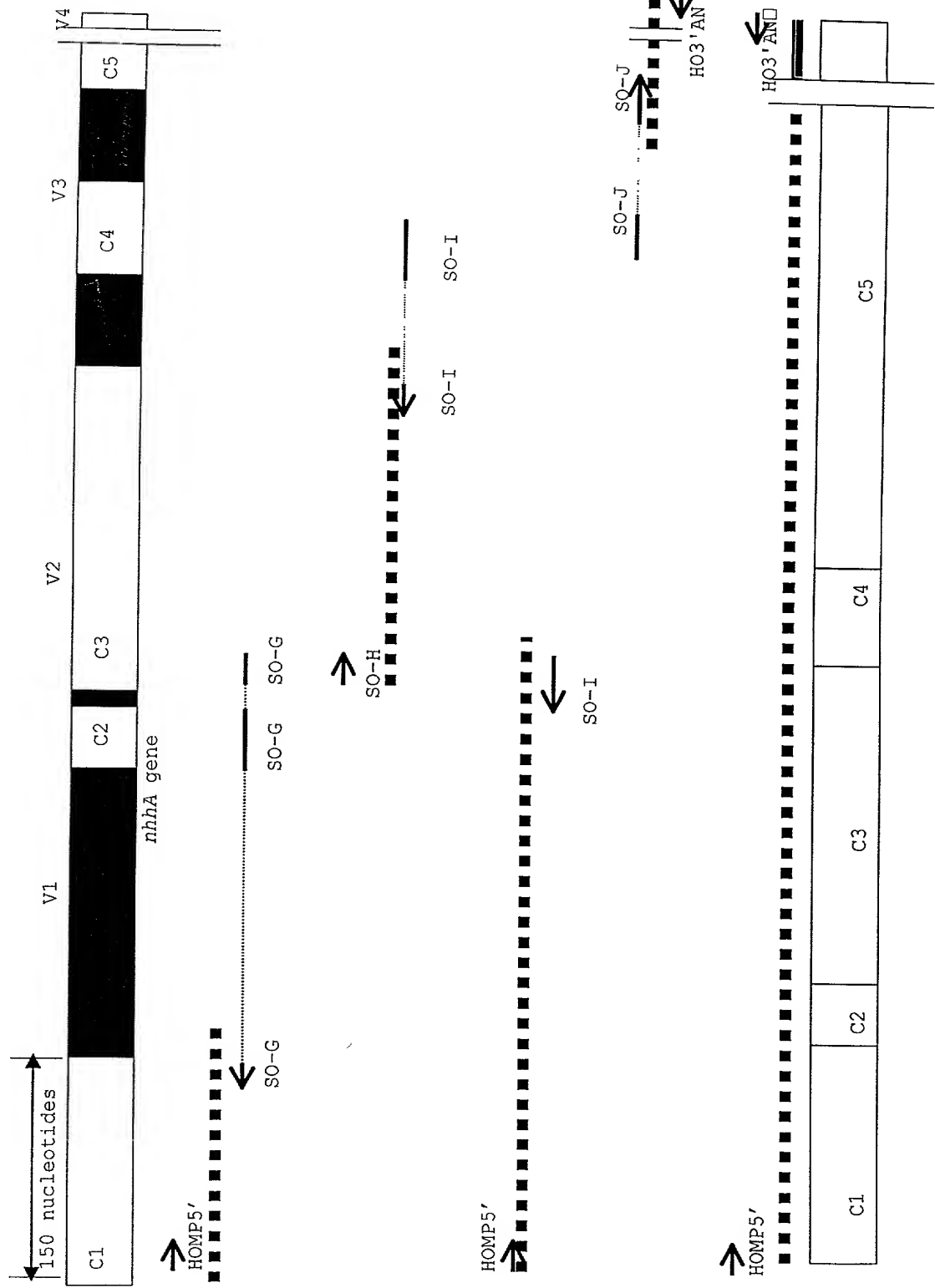


FIG. 4C

1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
 51 ANNETDLTSV GTEKLSFSAN GNKVNITS DT KGLNFAKETA GTNGD TT VHL
 101 NGIGSTLTDT LLNTGATTNV TNDNVT DDEK KRAASVKDVL NAGWNIKGVK
 151 PGT TASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS
 201 VIKEDGKLV TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKT TTA
 251 NGQTGQADKF ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA
 301 LNVNQLQNSG WNLD SKAVAG SSGKVISGNV SPSKGKMD ET VNINAGNNIE
 351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV
 401 RITNVAPGVK EGDVTNVAQL KGVAQN LNNR IDNVDGNARA GIAQAIATAG
 451 LVQAYLP GKS MMAIGGGTYR GEAGYAIGYS SISDGGNWII KG TASGNSRG
 501 HFGASASVGY QW*

FIG. 5A

1 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCCTCA ATGCATGGGT
 51 CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT
 151 GCTAACAAATG AAACAGATCT GACCAAGTGT GGAAC TGAA AATTATCGTT
 201 TAGCGCAAAC GGCAATAAAG TCAACATCAC AAGCGACACC AAAGGCTTGA
 251 ATTTTGCGAA AGAAACGGCT GGGACGAACG GCGACACCAC GGTTCATCTG
 301 AACGGTATTG GTTCGACTTT GACCGATACG CTGCTGAATA CCGGAGCGAC
 351 CACAAACGTA ACCAACGACA ACGTTACCGA TGACGAGAAA AAACGTGCGG
 401 CAAGCGTTAA AGACGTATTA AACGCTGGCT GGAACATTAA AGGCGTTAAA
 451 CCCGGTACAA CAGCTTCCGA TAACGTTGAT TTCGTCCGCA CTTACGACAC
 501 AGTCGAGTTC TTGAGCGCAG ATACGAAAAC AACGACTGTT AATGTGGA
 551 GCAAAGACAA CGGCAAGAAA ACCGAAGTTA AAATCGGTGC GAAGACTTCT
 601 GTTATTAAAG AAAAAGACGG TAAGTTGGTT ACTGGTAAAG ACAAAGGCGA
 651 GAATGGTTCT TCTACAGACG AAGGCGAAGG CTTAGTGACT GCAAAAGAAG
 701 TGATTGATGC AGTAAACAAG GCTGGTTGGA GAATGAAAAC AACAAACCGT
 751 AATGGTCAA CAGGTCAAGC TGACAAGTTT GAAACCGTTA CATCAGGCAC
 801 AAATGTAACC TTTGCTAGTG GTAAAGGTAC AACTGCGACT GTAAGTAAAG
 851 ATGATCAAGG CAACATCACT GTTATGTATG ATGTAAATGT CGGCGATGCC
 901 CTAAACGTCA ATCAGCTGCA AAACAGCGGT TGGAATTTGG ATTCCAAAGC
 951 GGTTCGAGGT TCTTCGGGCA AAGTCATCAG CGGCAATGTT TCGCCGAGCA
 1001 AGGGAAAGAT GGATGAAACC GTCAACATTA ATGCCGGCAA CAACATCGAG
 1051 ATTACCCGCA ACGGTAAAAA TATCGACATC GCCACTTCGA TGACCCCGCA
 1101 GTTTTCCAGC GTTTCGCTCG GCGCGGGGGC GGATGCGCCC ACTTTGAGCG
 1151 TGGATGGGGA CGCATTGAAT GTCGGCAGCA AGAAGGACAA CAAACCCGTC
 1201 CGCATTACCA ATGTCGCCCC GGGCGTTAAA GAGGGGGATG TTACAAACGT
 1251 CGCACAACTT AAAGGCGTGG CGCAAACTT GAACAACCGC ATCGACAATG
 1301 TGGACGGCAA CGCGCGTGCG GGCATCGCCC AAGCGATTGC AACCGCAGGT
 1351 CTGGTTCAGG CGTATTTGCC CGGCAAGAGT ATGATGGCGA TCGGCGGCGG
 1401 CACTTATCGC GGCGAAGCCG GTTACGCCAT CGGCTACTCC AGTATTTCCG
 1451 ACGGCGGAAA TTGGATTATC AAAGGCACGG CTTCCGGCAA TTCGCGCGCG
 1501 CATTTGCGTG CTTCCGCATC TGTCGGTTAT CAGTGGTAA

FIG. 5B

```

1  MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVQAN
51  ATDETGLINV ETEKLSFGAN GKKVNIISDT KGLNFAKETA GTNGDTTVHL
101 NGIGSTLTDM LLNTGATTNV TNDNVTDDK KRAASVKDVL NAGWNIKGVK
151 PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS
201 VIKKDGKLV TGKGKGNGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA
251 NGQTGQADKF ETVTSGTKVT FASGNGTTAT VSKDDQGNIT VKYDVNVGDA
301 LNVNQLQNSG WNLDSKAVAG SSGKVISGNV SPSKGKMDT VNINAGNNIE
351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDDEGAL NVGSKDANKP
401 VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN RIDNVNGNAR AGIAQAIATA
451 GLVQAYLPGK SMMAIGGGTY LGEAGYAIGY SSISAGGNWI IKGTASGNSR
501 GHFGASASVG YQW*

```

FIG. 6A

```

1  ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCCTCA ATGCCTGGGT
51  CGCCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG
101 TGAAGACCGC CGTATTGGCG ACGTGTGT TTGCAACGGT TCAGGCAAT
151 GCTACCGATG AAACAGGCCT GATCAATGTT GAAACTGAAA AATTATCGTT
201 TGGCGCAAAAC GGCAAGAAAG TCAACATCAT AAGCGACACC AAAGGCTTGA
251 ATTTTCGCGAA AGAAACGGCT GGGACGAACG GCGACACCAC GGTTCATCTG
301 AACGGTATCG GTTCGACTTT GACCGATATG CTGCTGAATA CCGGAGCGAC
351 CACAAACGTA ACCAACGACA ACGTTACCGA TGACGAGAAA AAACGTGCGG
401 CAAGCGTTAA AGACGTATTA AACGCAGGCT GGAACATTAA AGGCGTTAAA
451 CCCGGTACAA CAGCTTCCGA TAACGTTGAT TTCGTCCGCA CTTACGACAC
501 AGTCGAGTTC TTGAGCGCAG ATACGAAAAC AACGACTGTT AATGTGGAAA
551 GCAAAGACAA CGGCAAGAAA ACCGAAGTTA AAATCGGTGC GAAGACTTCT
601 GTTATTAAAG AAAAAGACGG TAAGTTGGTT ACTGGTAAAG GCAAAGGCGA
651 GAATGGTTCT TCTACAGACG AAGGCGAAGG CTTAGTGACT GCAAAGAAG
701 TGATTGATGC AGTAAACAAG GCTGGTTGGA GAATGAAAAC AACAAACCGCT
751 AATGGTCAAA CAGGTCAAGC TGACAAGTTT GAAACCGTTA CATCAGGCAC
801 AAAAGTAACC TTTGCTAGTG GTAATGGTAC AACTGCGACT GTAAGTAAAG
851 ATGATCAAGG CAACATCACT GTTAAGTATG ATGTAAATGT CGGCGATGCC
901 CTAAACGTCA ATCAGCTGCA AAACAGCGGT TGGAAATTTG ATTCCAAAGC
951 GGTTCGAGGT TCTTCGGGCA AAGTCATCAG CGGCAATGTT TCGCCGAGCA
1001 AGGGAAAGAT GGATGAAACC GTCAACATTA ATGCCGGCAA CAACATCGAG
1051 ATTACCCGCA ACGGCAAAAA TATCGACATC GCCACTTCGA TGACCCCGCA
1101 ATTTTCCAGC GTTTCGCTCG GCGCGGGGGC GGATGCGCCC ACTTTAAGCG
1151 TGGATGACGA GGGCGCGTTG AATGTCGGCA GCAAGGATGC CAACAAACCC
1201 GTCCGCATTA CCAATGTCGC CCCGGGCGTT AAAGAGGGGG ATGTTACAAA
1251 CGTCGCGCAA CTTAAAGGTG TGGCGCAAAA CTTGAACAAC CGCATCGACA
1301 ATGTGAACGG CAACGCGCGT GCGGGCATCG CCCAAGCGAT TGCAACCGCA
1351 GGTCTGGTTC AGGCGTATCT GCGGCGCAAG AGTATGATGG CGATCGGCGG
1401 CGGCACTTAT CTCGGCGAAG CCGGTTATGC CATCGGCTAC TCAAGCATTT
1451 CCGCCGGCGG AAATTGGATT ATCAAAGGCA CGGCTTCCGG CAATTCGCGC
1501 GGCCATTTTC GTGCTTCCGC ATCTGTCGGT TATCAGTGGT AA

```

FIG. 6B

1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAFLA TLLFATVQAS
 51 ANNVDVFRY DTVEFLSADT KTTTVNVESE DNGKKTEVKI GAKTSVIKEK
 101 DGKLVTKGDK GENSSSTDEG EGLVTAKEVI DAVNKAGWRM KTTTANGQTG
 151 QADKFETVTS GTNVTFASGK GTTATVSKDD QGNITVMYDV NVGDALNVNQ
 201 LQNSGWNLDS KAVAGSSGKV ISGNVSPSKG KMDET VNINA GNNIEITRNG
 251 KNIDIATSMT PQFSSVSLGA GADAPTLSDV GDALNVGSKK DNKPVRIITNV
 301 APGVKEGDVT NVAQLKGVAQ NLNNRIDNVD GNARAGIAQA IATAGLVQAY
 351 LPGKSMMIAIG GGTyrGEAGY AIGYSSISDG GNWIIKGTAS GNSRGHFGAS
 401 ASVGYQW*

FIG. 7A

1 ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCATGGGT
 51 CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT
 151 GCTAACACCG TTGATTTCTG CCGCACTTAC GACACAGTCG AGTTCCTGAG
 201 CGCAGATACG AAAACAACGA CTGTTAATGT GGAAAGCAAA GACAACGGCA
 251 AGAAAAACCGA AGTTAAAATC GGTGCGAAGA CTTCTGTTAT TAAAGAAAAA
 301 GACGGTAAGT TGGTTACTGG TAAAGACAAA GGCGAGAATG GTTCTTCTAC
 351 AGACGAAGGC GAAGGCTTAG TGAAGTCAAA AGAAGTGATT GATGCAGTAA
 401 ACAAGGCTGG TTGGAGAATG AAAACAACAA CCGCTAATGG TCAAACAGGT
 451 CAAGCTGACA AGTTTGAAAC CGTTACATCA GGCACAAATG TAACCTTTGC
 501 TAGTGGTAAA GGTACAACCTG CGACTGTAAG TAAAGATGAT CAAGGCAACA
 551 TCACTGTTAT GTATGATGTA AATGTCGGCG ATGCCCTAAA CGTCAATCAG
 601 CTGCAAAACA GCGGTTGGAA TTGGATTCC AAAGCGGTTG CAGGTTCTTC
 651 GGGCAAAGTC ATCAGCGGCA ATGTTTCGCC GAGCAAGGGA AAGATGGATG
 701 AAACCGTCAA CATTAAATGCC GGCAACAACA TCGAGATTAC CCGCAACGGT
 751 AAAAAATATCG ACATCGCCAC TTCGATGACC CCGCAGTTTT CCAGCGTTTC
 801 GCTCGGCGCG GGGGCGGATG CGCCCACTTT GAGCGTGGAT GGGGACGCAT
 851 TGAATGTCGG CAGCAAGAAG GACAACAAAC CCGTCCGCAT TACCAATGTC
 901 GCCCCGGGCG TTAAAGAGGG GGATGTTACA AACGTCGCAC AACTTAAAGG
 951 CGTGCGCGAA AACTTGAACA ACCGCATCGA CAATGTGGAC GGCAACGCGC
 1001 GTGCGGGCAT CGCCCAAGCG ATTGCAACCG CAGGTCTGGT TCAGGCGTAT
 1051 TTGCCCCGGA AGAGTATGAT GGCGATCGGC GCGGCGACTT ATCGCGGCGA
 1101 AGCCGGTTAC GCCATCGGCT ACTCCAGTAT TTCCGACGGC GGAAATTGGA
 1151 TTATCAAAGG CACGGCTTCC GGCAATTCGC GCGGCCATTT CGGTGCTTCC
 1201 GCATCTGTCC GTTATCAGTG GTAA

FIG. 7B

1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
 51 ANRAASVKDV LNAGWNIKGV KPGTTASDNV DFVRTYDTVE FLSADTKTTT
 101 VNVESKDNGK KTEVKIGAKT SVIKEKDGKL VTGKDKGENG SSTDEGEGLV
 151 TAKEVIDAVN KAGWRMKTIT ANGQTQADK FETVTSGTNV TFASGKGTTA
 201 TVSKDDQGNi TVMYDVNVGD ALNVNQLQNS GWNLD SKAVA GSSGKVISGN
 251 VSPSKGKMDE TVNINAGNNI EITRNGKNID IATSMTPQFS SVSLGAGADA
 301 PTLSDVDG DAL NVGSKKDNKP VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN
 351 RIDNVDGNAR AGIAQAIATA GLVQAYLP GK SMMAIGGGTY RGEAGYAIGY
 401 SSISDGGNWI IKGTASGNSR GHFGASASVG YQW*

FIG. 8A

1 ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCATGGGT
 51 CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT
 151 GCTAACCGTG CGGCAAGCGT TAAAGACGTA TTAAACGCTG GCTGGAACAT
 201 TAAAGGCGTT AAACCCGGTA CAACAGCTTC CGATAACGTT GATTTTCGTCC
 251 GCACTTACGA CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAACGACT
 301 GTTAATGTGG AAAGCAAAGA CAACGGCAAG AAAACCGAAG TTAAATCGG
 351 TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
 401 AAGACAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG
 451 ACTGCAAAAG AAGTGATTGA TGCAGTAAAC AAGGCTGGTT GGAGAATGAA
 501 AACAAACACC GCTAATGGTC AAACAGGTCA AGCTGACAAG TTTGAAACCG
 551 TTACATCAGG CACAAATGTA ACCTTTGCTA GTGGTAAAGG TACAACGCG
 601 ACTGTAAAGTA AAGATGATCA AGGCAACATC ACTGTTATGT ATGATGTAAA
 651 TGTCGGCGAT GCCCTAAACG TCAATCAGCT GCAAAAACAGC GGTTGGAATT
 701 TGGATTCCAA AGCGGTTGCA GGTCTTTCGG GCAAAGTCAT CAGCGGCAAT
 751 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCCG
 801 CAACAACATC GAGATTACCC GCAACGGTAA AAATATCGAC ATCGCCACTT
 851 CGATGACCCC GCAGTTTTCC AGCGTTTCGC TCGGCGCGGG GGCGGATGCG
 901 CCCACTTTGA GCGTGGATGG GGACGCATTG AATGTCGGCA GCAAGAAGGA
 951 CAACAAACCC GTCCGCATTA CCAATGTCGC CCCGGGCGTT AAAGAGGGGG
 1001 ATGTTACAAA CGTCGCACAA CTTAAAGGCG TGGCGCAAAA CTTGAACAAC
 1051 CGCATCGACA ATGTGGACGG CAACGCGCGT GCGGGCATCG CCCAAGCGAT
 1101 TGCAACCGCA GGTCTGGTTC AGGCGTATTT GCCCGCAAG AGTATGATGG
 1151 CGATCGGCGG CGGCACTTAT CGCGGCGAAG CCGGTTACGC CATCGGCTAC
 1201 TCCAGTATTT CCGACGGCGG AAATTGGATT ATCAAAGGCA CGGCTTCCGG
 1251 CAATTGCGCG GGCATTTCG GTGCTTCCGC ATCTGTGGT TATCAGTGGT
 1301 AA

FIG. 8B

FIG. 9A

FIG. 9B

	1				50
H41	<u>MNKIYRIWN</u>	<u>SALNAWVAVS</u>	<u>ELTRNHTKRA</u>	<u>SATVKTAVLA</u>	<u>TLLFATVOAN</u>
PMC21	<u>MNKIYRIWN</u>	<u>SALNAWVVVS</u>	<u>DLTRNHTKRA</u>	<u>SATVNTAVLA</u>	<u>TLLFATVOAS</u>
H41Studel	<u>MNKIYRIWN</u>	<u>SALNAWVAVS</u>	<u>ELTRNHTKRA</u>	<u>SATVKTAVLA</u>	<u>TLLFATVOAN</u>
PMC21Bgldel	<u>MNKIYRIWN</u>	<u>SALNAWVVVS</u>	<u>ELTRNHTKRA</u>	<u>SATVKTAVLA</u>	<u>TLLFATVOAS</u>
PMC21C1C5	<u>MNKIYRIWN</u>	<u>SALNAWVVVS</u>	<u>ELTRNHTKRA</u>	<u>SATVKTAVLA</u>	<u>TLLFATVOAS</u>
	C1				
	51				100
H41	<u>ATDED...EEE</u>	<u>ELESVQRS.V</u>	<u>VGSIQASMEG</u>	<u>SVELET...I</u>	<u>SLSMTNDSKE</u>
PMC21	<u>ANNEEQEYI</u>	<u>YLHPVQRTVA</u>	<u>VLIVNSDKEG</u>	<u>AGEKEKVEEN</u>	<u>SDWAVYFNEK</u>
H41Studel	<u>ATDE.....</u>	<u>.....</u>	<u>.....</u>	<u>.....</u>	<u>.....</u>
PMC21Bgldel	<u>ANNE.....</u>	<u>.....</u>	<u>.....</u>	<u>.....</u>	<u>.....</u>
PMC21C1C5	<u>AN.....</u>	<u>.....</u>	<u>.....</u>	<u>.....</u>	<u>.....</u>
	V1				
	101				150
H41	<u>FVDPYIVVTL</u>	<u>KAGDNLKIKO</u>	<u>N.TNENTNAS</u>	<u>SFTYSLKKDL</u>	<u>TGLINVETEK</u>
PMC21	<u>GVLTAIREITL</u>	<u>KAGDNLKIKO</u>	<u>NGTN.....</u>	<u>.FTYSLKKDL</u>	<u>TDLTSGVTEK</u>
H41Studel	<u>.....</u>	<u>.....</u>	<u>.....</u>	<u>.....</u>	<u>TGLINVETEK</u>
PMC21Bgldel	<u>.....</u>	<u>.....</u>	<u>.....</u>	<u>.....</u>	<u>TDLTSGVTEK</u>
PMC21C1C5	<u>.....</u>	<u>.....</u>	<u>.....</u>	<u>.....</u>	<u>.....</u>
	V1	C2	V2	C3	
	151				200
H41	<u>LSFGANGKKV</u>	<u>NIISDTKGLN</u>	<u>FAKETAGTNG</u>	<u>DTTVHLNGIG</u>	<u>STLTDMLLNT</u>
PMC21	<u>LSFSAHGNKV</u>	<u>NITSDTKGLN</u>	<u>FAKETAGTNG</u>	<u>DTTVHLNGIG</u>	<u>STLTDLLNT</u>
H41Studel	<u>LSFGANGKKV</u>	<u>NIISDTKGLN</u>	<u>FAKETAGTNG</u>	<u>DTTVHLNGIG</u>	<u>STLTDMLLNT</u>
PMC21Bgldel	<u>LSFSAHGNKV</u>	<u>NITSDTKGLN</u>	<u>FAKETAGTNG</u>	<u>DTTVHLNGIG</u>	<u>STLTDLLNT</u>
PMC21C1C5	<u>.....</u>	<u>.....</u>	<u>.....</u>	<u>.....</u>	<u>.....</u>
		C3		V3	
	201				250
H41	<u>GATTNVNTDN</u>	<u>VTDDEKKRAA</u>	<u>SVKDVLNAGW</u>	<u>NIKGVKPGTT</u>	<u>ASDNVDFVRT</u>
PMC21	<u>GATTNVNTDN</u>	<u>VTDDEKKRAA</u>	<u>SVKDVLNAGW</u>	<u>NIKGVKPGTT</u>	<u>ASDNVDFVRT</u>
H41Studel	<u>GATTNVNTDN</u>	<u>VTDDEKKRAA</u>	<u>SVKDVLNAGW</u>	<u>NIKGVKPGTT</u>	<u>ASDNVDFVRT</u>
PMC21Bgldel	<u>GATTNVNTDN</u>	<u>VTDDEKKRAA</u>	<u>SVKDVLNAGW</u>	<u>NIKGVKPGTT</u>	<u>ASDNVDFVRT</u>
PMC21C1C5	<u>.....</u>	<u>.....</u>	<u>.....</u>	<u>.....</u>	<u>...NVDFVRT</u>
	V3	C4	V4	C5	
	251				300
H41	<u>YDTVEFLSAD</u>	<u>TKTTTVNVES</u>	<u>KDNGKKTEVK</u>	<u>IGAKTSVIKE</u>	<u>KDGKLVTKGK</u>
PMC21	<u>YDTVEFLSAD</u>	<u>TKTTTVNVES</u>	<u>KDNGKKTEVK</u>	<u>IGAKTSVIKE</u>	<u>KDGKLVTKGD</u>
H41Studel	<u>YDTVEFLSAD</u>	<u>TKTTTVNVES</u>	<u>KDNGKKTEVK</u>	<u>IGAKTSVIKE</u>	<u>KDGKLVTKGK</u>
PMC21Bgldel	<u>YDTVEFLSAD</u>	<u>TKTTTVNVES</u>	<u>KDNGKKTEVK</u>	<u>IGAKTSVIKE</u>	<u>KDGKLVTKGD</u>
PMC21C1C5	<u>YDTVEFLSAD</u>	<u>TKTTTVNVES</u>	<u>KDNGKKTEVK</u>	<u>IGAKTSVIKE</u>	<u>KDGKLVTKGD</u>
	C5				
	301				350
H41	<u>KGENGSSTDE</u>	<u>GEGLVTAKEV</u>	<u>IDAVNKAGWR</u>	<u>MKTTTANGQT</u>	<u>GQADKFETVT</u>
PMC21	<u>KGENGSSTDE</u>	<u>GEGLVTAKEV</u>	<u>IDAVNKAGWR</u>	<u>MKTTTANGQT</u>	<u>GQADKFETVT</u>
H41Studel	<u>KGENGSSTDE</u>	<u>GEGLVTAKEV</u>	<u>IDAVNKAGWR</u>	<u>MKTTTANGQT</u>	<u>GQADKFETVT</u>
PMC21Bgldel	<u>KGENGSSTDE</u>	<u>GEGLVTAKEV</u>	<u>IDAVNKAGWR</u>	<u>MKTTTANGQT</u>	<u>GQADKFETVT</u>
PMC21C1C5	<u>KGENGSSTDE</u>	<u>GEGLVTAKEV</u>	<u>IDAVNKAGWR</u>	<u>MKTTTANGQT</u>	<u>GQADKFETVT</u>
	C5				
	351				400
H41	<u>SGTKVTFASG</u>	<u>NGTTATVSKD</u>	<u>DOGNITVKYD</u>	<u>VNVGDALNVN</u>	<u>QLQNSGWNLD</u>
PMC21	<u>SGTNVTFASG</u>	<u>KGTTATVSKD</u>	<u>DOGNITVMYD</u>	<u>VNVGDALNVN</u>	<u>QLQNSGWNLD</u>
H41Studel	<u>SGTKVTFASG</u>	<u>NGTTATVSKD</u>	<u>DOGNITVKYD</u>	<u>VNVGDALNVN</u>	<u>QLQNSGWNLD</u>
PMC21Bgldel	<u>SGTNVTFASG</u>	<u>KGTTATVSKD</u>	<u>DOGNITVMYD</u>	<u>VNVGDALNVN</u>	<u>QLQNSGWNLD</u>
PMC21C1C5	<u>SGTNVTFASG</u>	<u>KGTTATVSKD</u>	<u>DOGNITVMYD</u>	<u>VNVGDALNVN</u>	<u>QLQNSGWNLD</u>
	C5				

FIG. 10

401 450
H41 SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
PMC21 SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
H41Studel SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
PMC21Bgldel SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
PMC21C1C5 SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
C5

451 500
H41 TPQFSSVSLG AGADAPTLVS DDEGALNVGS KDANKPVRLT NVAPGVKEGD
PMC21 TPQFSSVSLG AGADAPTLVS DG.DALNVGS KKDANKPVRLT NVAPGVKEGD
H41Studel TPQFSSVSLG AGADAPTLVS DDEGALNVGS KDANKPVRLT NVAPGVKEGD
PMC21Bgldel TPQFSSVSLG AGADAPTLVS DG.DALNVGS KKDANKPVRLT NVAPGVKEGD
PMC21C1C5 TPQFSSVSLG AGADAPTLVS DG.DALNVGS KKDANKPVRLT NVAPGVKEGD
C5

501 550
H41 VTNVAQLKGV AQNLNNRIDN VNGNARAGIA QAIATAGLVQ AYLPGKSMMA
PMC21 VTNVAQLKGV AQNLNNRIDN VDGNNARAGIA QAIATAGLVQ AYLPGKSMMA
H41Studel VTNVAQLKGV AQNLNNRIDN VNGNARAGIA QAIATAGLVQ AYLPGKSMMA
PMC21Bgldel VTNVAQLKGV AQNLNNRIDN VDGNNARAGIA QAIATAGLVQ AYLPGKSMMA
PMC21C1C5 VTNVAQLKGV AQNLNNRIDN VDGNNARAGIA QAIATAGLVQ AYLPGKSMMA
C5

551 600
H41 IGGGTYLGEA GYAIGYSSIS AGGNWIIKGT ASGNSRGHFG ASASVGYQW.
PMC21 IGGGTYRGEA GYAIGYSSIS DGGNWIIGKT ASGNSRGHFG ASASVGYQW.
H41Studel IGGGTYLGEA GYAIGYSSIS AGGNWIIKGT ASGNSRGHFG ASASVGYQW.
PMC21Bgldel IGGGTYRGEA GYAIGYSSIS DGGNWIIGKT ASGNSRGHFG ASASVGYQW.
PMC21C1C5 IGGGTYRGEA GYAIGYSSIS DGGNWIIGKT ASGNSRGHFG ASASVGYQW.
C5

FIG. 10

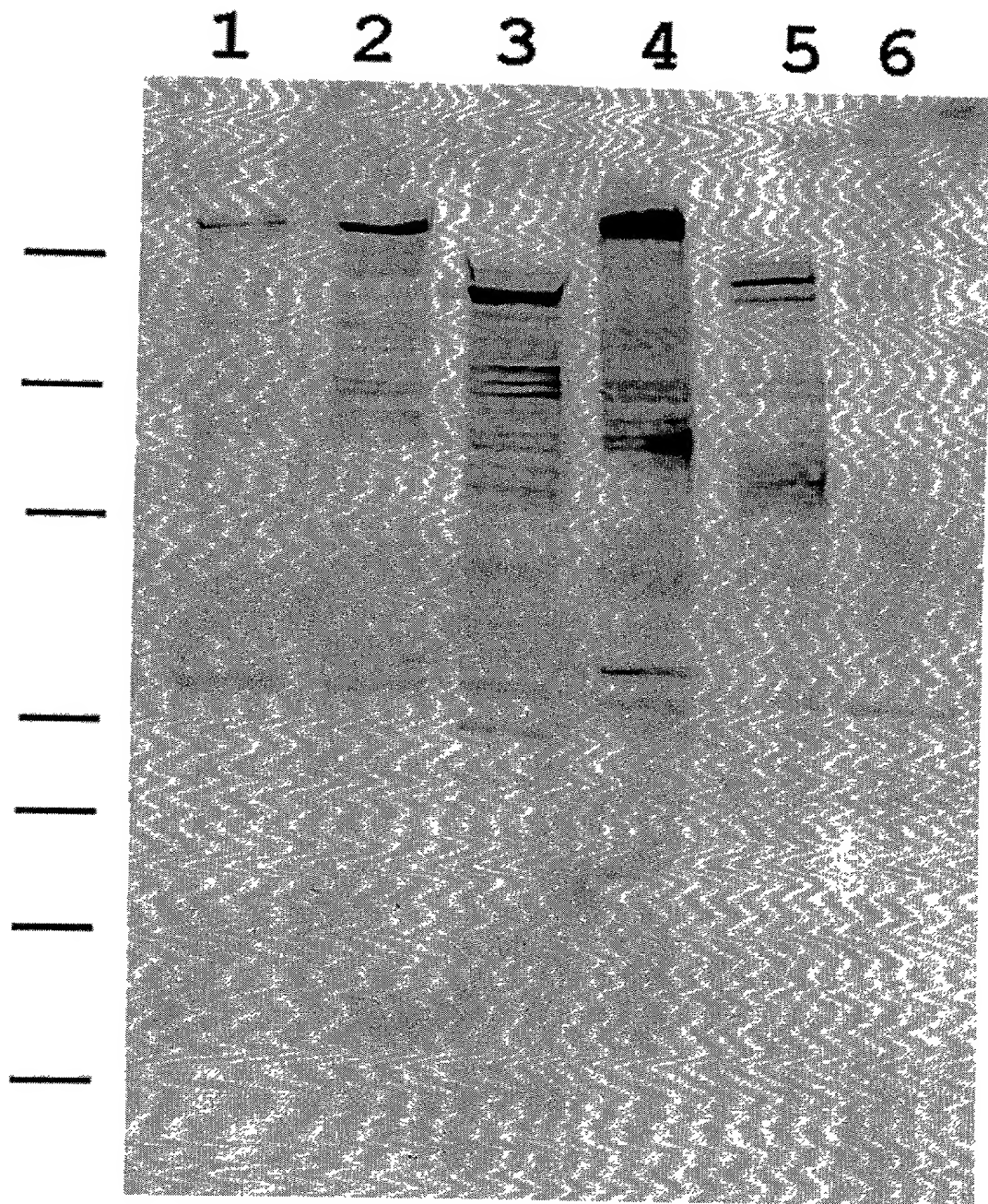


FIG. 11

TOP 40" 286T/260

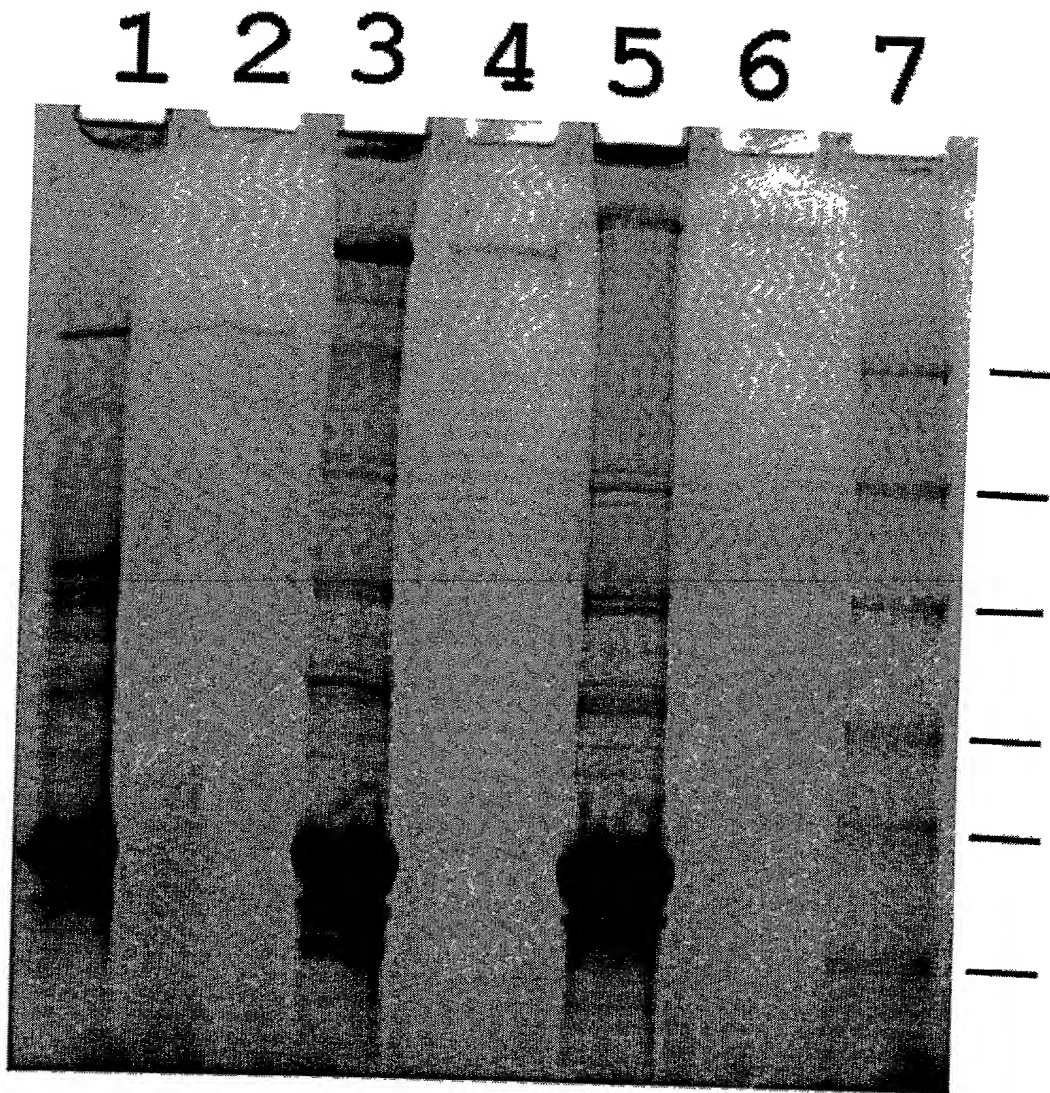
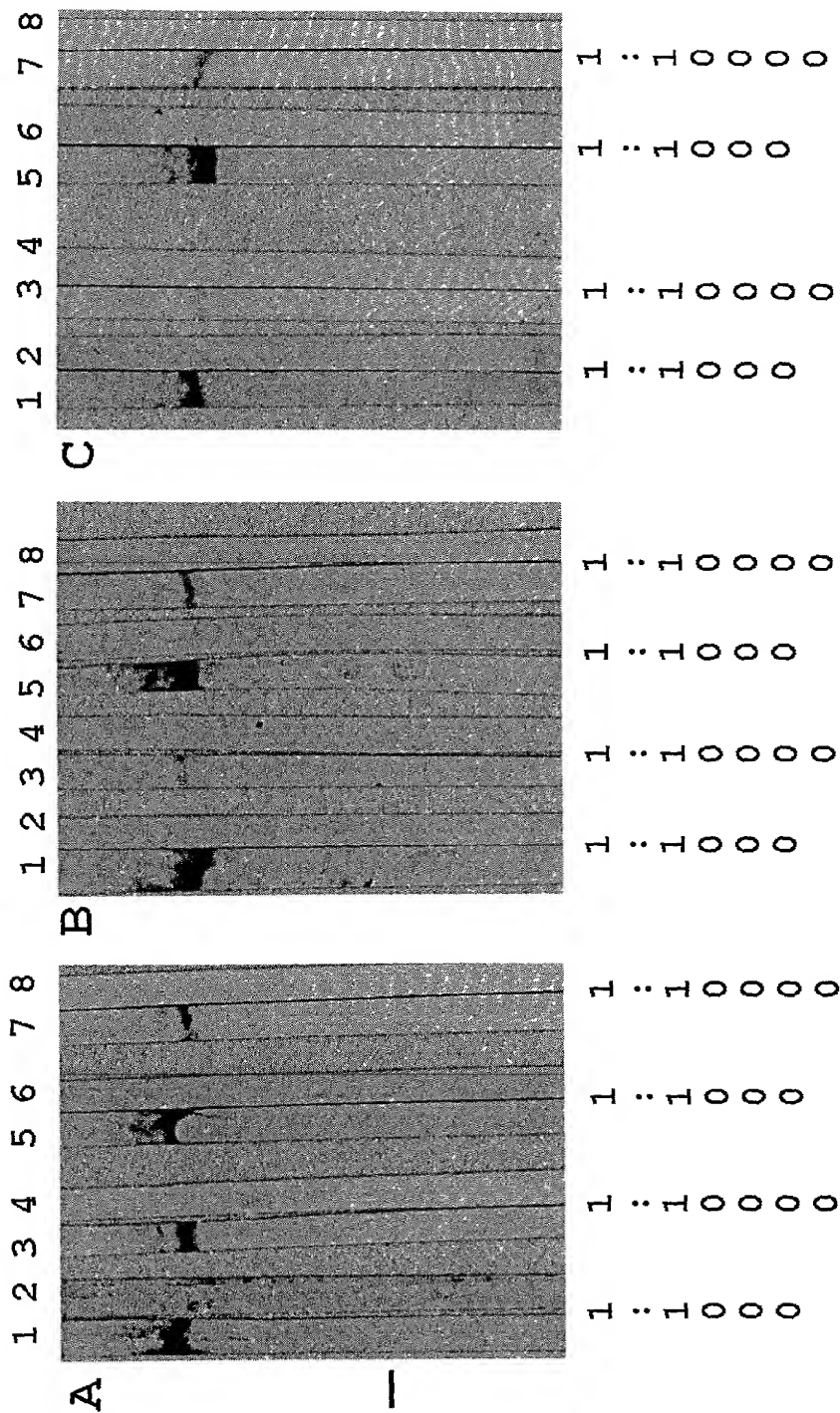


FIG. 12

TOP OF 288T/60



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FIG. 13

52 NNEEQEEYL YLHPVQRTVA VLIVNSDKEG AGEKEKVEEN SDWAVYFNEK
 101 GVLTAAREITL KAGDNLKIKQ NGTNFTYSLK KDLTDLTSVG TEKLSFSAHG
 151 NKVNITS DTK GLNFAKETAG TNGDTTVHLN GIGSTLTDTL LNTGATTNVT
 201 NDNVTDDEKK RAASVKDVLN AGWNIKGVPK GTTASDNVDF VRTYDTVEFL
 251 SADTKTTTVN VESKDNGKKT EVKIGAKTSV IKEKDGLVT GKDKGENGSS
 301 TDEGEGLVTA KEVIDAVNKA GWRMKTTTAN GQTGQADKFE TVTSGTNVTF
 351 ASGKGTTATV SKDDQGNITV MYDVNVGDAL NVNQLQNSGW NLDSKAVAGS
 401 SGKVISGNVS PSKGKMDTV NINAGNNIEI TRNGKNIDIA TSMT PQFSSV
 451 SLGAGADAPT LSVDGDALNV GSKKDNKPVR ITNVAPGVKE GDVTNVAQLK
 501 GVAQNLNNRI DNV DGNARAG IAQAIATAGL VQAYLPGKSM MAIGGGTYRG
 551 EAGYAIGYSS ISDGGNWIIK GTASGNSRGH FGASASVG YQ W*

FIG. 14A

52 TDEDEEEEL ESVQRSVVGS IQASMEGSVE LETISLSMTN DSKEFVDPYI
 101 VVTLKAGDNL KIKQNTNENT NASSFTYSLK KDLTGLINVE TEKLSFGANG
 151 KKVNIISDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDML LNTGATTNVT
 201 NDNVTDDEKK RAASVKDVLN AGWNIKGVPK GTTASDNVDF VRTYDTVEFL
 251 SADTKTTTVN VESKDNGKKT EVKIGAKTSV IKEKDGLVT GKDKGENGSS
 301 TDEGEGLVTA KEVIDAVNKA GWRMKTTTAN GQTGQADKFE TVTSGTKVTF
 351 ASGNGTTATV SKDDQGNITV KYDVNVGDAL NVNQLQNSGW NLDSKAVAGS
 401 SGKVISGNVS PSKGKMDTV NINAGNNIEI TRNGKNIDIA TSMT PQFSSV
 451 SLGAGADAPT LSVDDEGALN VGSKDANKPV RITNVAPGVK EGDVTNVAQL
 501 KGVAQNLNNR IDNVNGNARA GIAQAIATAG LVQAYLPGKS MMAIGGGTYL
 551 GEAGYAIGYS SISAGGNWII KGTASGNSRG HFGASASVG Y QW*

FIG. 14B

52 NNETDLTSV GTEKLSFSAN GNKVNITS DT KGLNFAKETA GTNGD TTVHL
 101 NGIGSTLTDT LLNTGATTNV TNDNVT DDEK KRAASVKDVL NAGWNIKGVK
 151 PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS
 201 VIKKDGKLV TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA
 251 NGQTGQADKF ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA
 301 LNVNQLQNSG WNLDKAVAG SSGKVISGNV SPSKGKMD ET VNINAGNNIE
 351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV
 401 RITNVAPGVK EGDVTNVAQL KGVAQN LNNR IDNV DGNARA GIAQAIATAG
 451 LVQAYLPGKS MMAIGGGTYR GEAGYAIGYS SISDGGNWII KG TASGNSRG
 501 HFGASASVGY QW*

FIG. 14C

52 TDETGLINV ETEKLSFGAN GKKVNIISDT KGLNFAKETA GTNGD TTVHL
 101 NGIGSTLTDM LLNTGATTNV TNDNVT DDEK KRAASVKDVL NAGWNIKGVK
 151 PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS
 201 VIKKDGKLV TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA
 251 NGQTGQADKF ETVTSGTKVT FASGNGTTAT VSKDDQGNIT VKYDVNVGDA
 301 LNVNQLQNSG WNLDKAVAG SSGKVISGNV SPSKGKMD ET VNINAGNNIE
 351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDDEGAL NVGSKDANKP
 401 VRITNVAPGV KEGDVTNVAQ LKGVAQN LNN RIDNVNGNAR AGIAQAIATA
 451 GLVQAYLPGK SMMAIGGGTY LG EAGYAIGY SSISAGGNWI IKGTASGNSR
 501 GHFGASASVG YQW*

FIG. 14D

FIG. 14E

FIG. 14F

FIG. 14G